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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2834.52 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-4
Perfect score: 1101
Sequence: 1 atgaagttacttacttacc.....caggtgttcagaanaataa 1101

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl1:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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7: gb_ph:*
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37: em_hcg_vrt:*
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40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	19.9	828	3	AB045179
2	217.4	19.7	808	3	AB045178
3	214.2	19.5	840	3	AB045172
4	213.4	19.4	710	3	AB045171
5	210.4	19.1	780	3	AB045168
6	208.4	18.9	774	3	AB045170
7	202	18.3	784	3	AB045167
8	201.2	18.3	781	3	AB045165
9	194.8	17.7	785	3	AB045177
10	194.2	17.6	1443	8	FSOKCH
11	194.2	17.6	1473	6	A21795
12	194.2	17.6	1473	6	A23637
13	194.2	17.6	1473	6	A23646
14	194.2	17.6	1473	6	A23955
15	194.2	17.6	1473	6	A23959
16	194.2	17.6	1473	6	A41660
17	194.2	17.6	1473	6	AR072922
18	194.2	17.6	1473	6	BD002249
19	194.2	17.6	1473	6	BD010853
20	194.2	17.6	1473	6	113885
21	194.2	17.6	1473	6	121317
22	194.2	17.6	1473	6	157984
23	191.2	17.4	759	3	AB045174
24	189.4	17.2	783	3	AB045173
25	188.6	17.1	761	3	AB045175
26	188.2	17.1	802	3	AB045176
27	187.6	17.0	798	3	AB045166
28	186.2	16.9	785	3	AB045169
29	181.2	16.5	1423	6	AR094309
30	178	16.2	927	6	AR094307
31	177.8	16.1	960	6	AR094305
32	177.8	16.1	1132	6	AR094315
33	177.2	16.1	924	6	A68074
34	177.2	16.1	924	6	AR163169
35	176.8	16.1	894	6	AR094306
36	174.4	15.8	919	6	A68072
37	174.4	15.8	919	6	AR163168
38	168.4	15.3	1418	8	PEQ277482
39	166.4	15.1	922	6	A68070
40	166.4	15.1	922	6	AR163167
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43	162	14.7	885	6	AR094316
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45	161.6	14.7	912	6	AR163170

ALIGNMENTS

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DEFINITION Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
AB045179
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE
AUTHORS
TITLE
Diverse genes of cellulase homologues of glycosyl hydrolase family

(E-mail: mohkuma@mailman.riken.go.jp, Tel: 66-48-467-9545,
Fax: 66-48-462-4672)

FEATURES
source Location/Qualifiers

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130484"
/clone="7-50"

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BASE COUNT 185 a 137 c 197 g 191 t

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Best Local Similarity 62.4%; Pred. No. 6.4e-46;
Matches 391; Conservative 0; Mismatches 221; Indels 15; Gaps 3;

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65 AGCGAAGAACACCCCGTATTGGGATTGTGCAAGCCGCTGCGGAAAAAAA 124
538 GCCAATGTCATCTCTCTGTCAGTCCGTAAACAGATGATGTCAGTCCCTT--AGT 594
125 GCTGCTTTACACAGCTCTGTGACACTTGTGCAAAAATGAGGACACAGAGATTGCGAC 184
595 GACAGCAATGTCAGAAAGTGGCTGTACCGTGTGTACAGTTACATGTGTAAACGACG 654
185 AATGACATGTAATCAGCTGTGTGATGTGAGAGAGATATATGTATGATCAAGCA 244
655 CCTGGGCTGTAAAGATATCTGATGTTTGGCTGCTGTCGCATCAAGTGTGT 714
245 CCATGGGAGTAAATGACTCTGTGCTGACGTTTGTGCTGACG---TTGCTGTGG 301
715 GGTGAATCTCGTGTGTGCTGTTCTTGTTCGACTTACTTCACTTCACTGCTGTTGCT 774
302 GGGGAAAGGAGAGCTGTGCAATGTGATGAGCTTAATCAACAGTGAACGAGTGAAT 361
775 GGTAAAGATGTTTACAGATCACTACGCTGATCTTGGCTCTCTACTGTGT 834
362 GGAAGAAATGTTGTGACAGTACACGACCAACCGGTGTGATCTTGGCTC-----G 412
835 GCTCACTTGTGCTGCAATGCCCCGGTGTGTGTGTATTTTCAATGTGTGCTCAAG 894
413 AATCAGTTTATCTTGGAATTCGGGTGAGAGTGTGATCTTAACGCTGACCCAG 472
895 CAATGGGTGCTCCCAATGAGCGTTGGGGCTGAGATACGAGTATTTCTTGCATCT 954
473 CAATCAGTGCACCTGTGATGAGAGGAGGAGCGGATATGAGAGTCTTCACTCCGAC 532
955 GACTGCTAGTCTTCTCTCCGCACTCAAGCTGTGTGATATGAGATTTCACTGTTT 1014
533 GAATGCTTCACTTCTCGGTGGGCTTCAAGCTGGGCTCAATGAGAGATTTGATGTTG 592
1015 AAGAACTGTATTAACCAAGATTAACAGGAGTACTGTCCCAAGGAATCACC 1074
593 CAATATGCCGATACCTTCAATCAATTTCAACCAAGTGAATGCTTGTGTGATTAAG 652
1075 GCCAAGACAGGTGTTCAAGAAATTA 1101
653 GCAAAAACCAATTGCAAGGACCTTA 679

RESULT 5
AB045168 780 bp mRNA linear INV 14-FEB-2001
LOCUS AB045168
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE

Direct Submission
Submitted (24-JUN-2003) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory, Hiroshima
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail: mohkuma@mailman.riken.go.jp, Tel: 66-48-467-9545,
Fax: 66-48-462-4672)

FEATURES
source Location/Qualifiers

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BASE COUNT 196 a 155 c 206 g 223 t

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Best Local Similarity 61.9%; Pred. No. 4e-45;
Matches 391; Conservative 0; Mismatches 226; Indels 15; Gaps 3;

472 TCTGTTAAGGTGTCATCTACTGTTATTGGATTGCTGTAAAGCCCTCTGAGTGGCC 531
64 TGTGACAGTGCAAAACGACCCGCTATTGGAGCTGTGCAAGCTCTGTGCTGGAA 123
532 GGTAAAGCCATGTCAGTCTCTGTCAAGCTCTGTAACAAAGATGTGCTACTGCCCT 591
124 GCCAAGCTGATGTAGCAAAACGATAGACACGTCGCAAAAGATGACACACTCGAGTT 183
592 AGTGAAGCAAT--GTCCAAAGTGGCTGTACGCTGTAAACATTCATGATGTAAAGAC 648
184 GCAAGCAAGATACGTAATAATCTGTGTGATGAGCGGTGACGCTTCAATGTAGAT 243
649 AACACGCTTGGCTGTAAAGATATCTGCTATGATTTGCTGCTGTCGCATCACT 708
244 CAATCCCGTGGGGCTGACAGATTTTACGCTTGGGATTTGCTGCTGACGACATTTCA 303
709 GGTGTGTGTAATCTCGTGTGCTGTTCTTGTTCGAATCTTCACTTCACTTCACTCT 768
304 GAGGTGAGAAAGCTCC--TGTGTATATTTTCAAGTTGATCTTACCTTGGCCCC 360
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361 GTTATGTGCAAGAGATGATGTTTCAAGTTTCAACACCGGAGGATCTCGGTTTCT 416
829 ACTGTGCTCACTTGTGCAATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 888
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889 TCCAAGCAATGGGCTCTCCCATGACGTTGGGGCTGAGATACGTTGATTTCTTCT 948

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Db      532  CGCAGTGAATCTCCAGCTTCTTGGGCTTCAGGCTGCTGCAGTGAAGATTTCAT 591
Oy      1009  TGGTTCAAGAAGCTGATTAACCAAGCATGACTTCAAGAAATTACCTGTCCCAAGGA 1068
Db      592  TGGTTCCAAATGCCGAGATCCGTCATGAATTAAGTGTGTCTGCTGCCCAAGTAG 651
Oy      1069  ATCAACGCCCAAGACAGGTTGTTCAAGAAATA 1100
Db      652  TTGATTCGAAAACCAATTGCAGACGCAATTA 683

RESULT 6
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LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION AB045170
ACCESSION AB045170.1 GI:8926972
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Ohoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2 (bases 1 to 774)
Ohkuma,M.
JOURNAL Direct Submission
TITLE Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroshima 2-1, Wako-shi, Saitama 351-0198, Japan
AUTHORS (E-mail:mohkumamailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
JOURNAL Location/Qualifiers
FEATURES
SOURCE
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BASE COUNT 179 a 144 c 212 g 239 t
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Best Local Similarity 61.7%; Pred. No. 14e-44;
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Oy      535  AAGGCCATGTCAAGTTCTCTGCTCAAGTCTGTAACAAAGATGCTGACTGCGCTT--- 591
Db      157  AAGGCTAATGTGACAAACGCTATTGATGATGCGCAAAAGATGTACCAAGAGTTGCA 216

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Oy      592  AGTGACAGCATATGTCCAAAGTGGCTGTAAACGCTGTAAACAGTTACATGTGTACAGAAC 651
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Oy      652  CAGCTTGGGCTGTAAACGATATCTTGGCTTATGCTTGGCTGCTGTCATCAGTGTGT 711
Db      277  TCTCCGTGGGGGTGCATATGATCTTTTGTCTGTGGGTTTGTCTGCGACGCGTTCAGGA 336
Oy      712  GGTGTGAATCTGCTGGTGTGCTTTCTTTTGTGCACTTATTCACCTTACCTGTGT 771
Db      337  GGTAGAGCGCTGCC---TGCTGCAATGTGTATGCAAGTTACATTCATCTTGCGCCAGTT 393
Oy      772  GCTGTAAAGATAGTGTATTCAGATCACTAACACTGCTGTGATCTTGGCTCTCTACT 831
Db      394  AATGGAAGAAGATGACTGTTCAGGTTACCAACACTGGGGGTGACCTTGTTCC----- 447
Oy      832  GGTGCTCATTTGACTTGCAATATGCCGGTGTGTGTGTGTAATTTCAATGTGTCTCC 891
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LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION AB045167
ACCESSION AB045167
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Ohoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2 (bases 1 to 784)
Ohkuma,M.
JOURNAL Direct Submission
TITLE Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroshima 2-1, Wako-shi, Saitama 351-0198, Japan
AUTHORS (E-mail:mohkumamailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
JOURNAL Location/Qualifiers
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 AB045177
 VERSION AB045177.1 GI:8926986
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 OHKO, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL MEDLINE 21020023
 REFERENCE 2 (bases 1 to 785)
 Ohkuma, M.
 Direct Submission
 Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirogawa 2-1, Wako-shi, Saitama 351-0198, Japan
 E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672
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 Db 81 ACAATCTCCTATTTGGATTGCTGCAAGAACTGTGGTGGTGAAGAAAGCCCATGTG 140
 Oy 547 AGTTCTCTGCAATCTCTGTAAACAAGATGCTGACCTCT--AGTACAGCAAT 603
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 Oy 664 GTAACGATTAATCTGCGATAGTCTTGTGCTGCTGCATACAGTGTGTGTAAATCT 723
 Db 261 GTAATTAATCTGATTAATCAAGCTTTGTGCTGAGC--TTGCTGTGGCGGTAGAGT 317
 Oy 724 CGCTGTGCTGCTTTCTTGTTCGAACTTCACTTCACTTCACTTGTGCTGTAAAG 783

Db 318 GGTGCTGTGCTGCTGCTCTATGATTTGACATTCACAAGTGGCGGTCACAAAGCAAT 377
 Oy 784 ATGGTATTCAGACACTACACTGATGATGATGATGATGATGATGATGATGATGATGAT 843
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 Db 609 GACATCCGAACATCAATTTACAGAGTTAGATGCCAGCTGAGATTTATGCCAAACC 668
 Oy 1084 GGTGTTCAAGAAATAA 1101
 Db 669 AATTGCAACGAGTTAA 686
 RESULT 10
 LOCUS FSOXCH 1443 bp mRNA linear PLN 28-APR-1995
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 ACCSSION L29381
 KEYWORDS K-family cellulase homologue; cellulase; homologue.
 SOURCE Fusarium oxysporum
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
 REFERENCE 1 (bases 1 to 1443)
 Sheppard, P.O., Grant, F.J., Oort, P.J., Sprecher, C.A., Foister, D.C., Hagen, F.S., Upshall, A., McKnight, G.D. and O'Hara, P.J.
 The use of conserved cellulase family-specific sequences to clone cellulase homologue cDNAs from Fusarium oxysporum
 Gene 150 (1), 163-167 (1994)
 JOURNAL MEDLINE 95047531
 PUBMED 7959045
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Db 129 GTGCTCTTCTGGAAGCGGTACTCTACTGATCTGGAATGCTGCAGACCTTCTGCT 188
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 Db 369 TCTCCGCTGCTCCGAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
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 Db 429 GCCCGGTCAAGGCGAAGAAATGATGCTCAAGTCAACCAACTGAGGTGATCTCGGC- 487
 QY 824 CTTTACTGCTGCTCACTTGTGCAATGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCT 883
 Db 488 -----GACAACTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 539
 QY 884 GTTCTCCAGCAATGAGGTGCTCCCAATGACGCTTGGGCTGCAATACGCTGATTT 943
 Db 540 GCTGACCTCTGAGTTGG-----CAAGCTCTCGCGGTGCTCCAGTACGGGGATCT 593
 QY 944 CTTTGTGATCTGCTGCTGCTGCTGCTTCTTCCGCTCTCAAGCTGCTGCTGCTGCTGCT 1003
 Db 594 CTTCCCGAAGGAGATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 653
 QY 1004 TCACTGCTGTAAGAGCTGATTAACCAAGCATGACTTACAGGAAGTTACTGCTTCCA 1063
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 QY 1064 AGGAATCAACGCCCAAGCAGTTG 1088
 Db 714 AGGCTCTCTCGACATCAGTGGATG 738

RESULT 11
 A21795 1473 bp mRNA linear PAT 20-SEP-1995
 LOCUS F.oxysporum mRNA for endonuclease component.
 DEFINITION A21795
 ACCESSION A21795
 VERSION A21795.1 GI:1246874
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.

FEATURES
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 97..1227
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BASE COUNT 343 a 453 c 337 g 340 t

ORIGIN

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
 Best Local Similarity 59.5%; Pred. No. 8,3e-41;
 Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

QY 464 GTGAGCTCTGTGTAACGCTGCTACTCTGCTTATTTGGAGTGTGCTGTAAGAGCTCTGTA 523
 Db 143 GTGCTCTTCTGGAAGCGGTACTCTACTGATCTGGAATGCTGCAAGCTCTTCTGCT 202
 QY 524 GCTGCCCCGTTAAGCCCAATGCTATCTCTGCTCAAGCTCTGTAACAAGATGCTCA 583
 Db 203 CTTGAGCGGAAGCTGCTGTCAACGGTGTGAAGGTGTGCTGCTTATGCTTATGCTTGA 262
 QY 584 CTGCCCCCTAGTACAGCAATGCTCAAAAGTGTGTAACGGTGTAAACAGTTACATGTGA 643
 Db 263 CCAATTTCCAAACCAATGCTGTCAACGGTGTGAAGGTGTGCTGCTTATGCTTATGCTTGA 322
 QY 644 AGCAACAACAGCTTGGGCTGTAAAGATATCTGCTAATGCTTGGCTGCTGCTCA 703
 Db 323 CCAACTACTCTCCCTGGGCTGTCAAGATGCTGCTCAAGCTTGGCTTGGCTGCTCAAGA 382
 QY 704 TCAGTGTGTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
 Db 383 TCTCCGCTGCTCCGAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442
 QY 764 CTTCTGCTGCTGTAAGAGATGCTTATCCAGTCACTCAACCTGCTGCTGCTGCTGCT 823
 Db 443 GCCCGGTCAAGGCGAAGAAATGATGCTCAAGTCAACCAACTGAGGTGATCTCGGC- 501
 QY 824 CTTTACTGCTGCTCACTTGTGCAATGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCT 883
 Db 502 -----GACAACTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 553
 QY 884 GTTCTCCAGCAATGAGGTGCTCCCAATGACGCTTGGGCTGCAATACGCTGATTT 943
 Db 554 GCTGACCTCTGAGTTGG-----CAAGCTCTCGCGGTGCTCCAGTACGGGGATCT 607
 QY 944 CTTTGTGATCTGCTGCTGCTGCTGCTTCTTCCGCTCTCAAGCTGCTGCTGCTGCTGCT 1003
 Db 608 CTTCCCGAAGGAGATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 667
 QY 1004 TCACTGCTGTAAGAGCTGATTAACCAAGCATGACTTACAGGAAGTTACTGCTTCCA 1063
 Db 668 TCGACTGCTGTAAGAGCTGATTAACCAAGCATGACTTACAGGAAGTTACTGCTTCCA 727
 QY 1064 AGGAATCAACGCCCAAGCAGTTG 1088
 Db 728 AGGCTCTCTCGACATCAGTGGATG 752

RESULT 12

A23637 1473 bp mRNA linear PAT 19-SEP-1995
 LOCUS F.oxysporum endoglucanase gene.
 DEFINITION A23637
 ACCESSION A23637.1 GI:832888
 VERSION A23637.1 GI:832888
 KEYWORDS endoglucanase.
 SOURCE Fusarium oxysporum.
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.

REFERENCE 1 (bases 1 to 1473)
 AUTHORS Convents,A.C., Busch,A. and Baeck,A.C.
 TITLE Determination of the endoglucanase gene of Fusarium oxysporum
 by using degenerate primers and high activity cellulase and softening
 clays

JOURNAL Patent: EP 0495258-A 3 22-JUL-1992;

THE PROCTER & GAMBLE COMPANY
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:5507"

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97.1227
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BASE COUNT 343 a 453 c 337 g 340 t

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
Best Local Similarity 59.5%; Pred. No. 8.3e-41;
Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

OY 464 GTGGTGCCTCTGTTAAGCGGTGCACTACTGTTATTGGGATTGCTTAAGGCTCTGTTA 523
DB 143 GTGGTGCCTCTGTTAAGCGGTGCACTACTGTTATTGGGATTGCTTAAGGCTCTGTTA 202
OY 524 GCTGCGCGGTAAAGCGCAATGTCTCTCTGCAAGTCTCTTAACAAGATGATGCA 583
DB 203 CTGGAGCGGAAGGCTGCTGCAACGCCCTGCTTAACCTTGATGAAGAACCAACC 262
OY 584 CTGCGCTTAAGTACAGCAATGTCCAAAGTGTGTAACGCTGTAACAGTTACATGTGTA 643
DB 263 CCATTTCCACACCAATGTCTGTAACGCTGTAAGGCTGTAAGGCTGTAAGGCTGTA 322
OY 644 ACGAACACAGCTTGGGCTGTAACGATTAATCTTGGCTTATGCTGCTGCTGCA 703
DB 323 CCAACTACTCTCTGCGGCTGTAACGATTAATCTTGGCTTATGCTGCTGCTGCA 382
OY 704 TCAAGTGTGTTGTAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 763
DB 383 TCTCCGGTGTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 442
OY 764 CTTCTGTTGTTGTAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 823
DB 443 GCCCGTCAAGGCGCAAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 501
OY 824 CCTCTACTGTTGCTCACTTGAATGCAATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 883
DB 502 -----GACAAACACTTCTGATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 553
OY 884 GTTCTCAAGCAATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 943
DB 554 GCTGCACTCTGAGTTGG-----CAAGGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 607
OY 944 CTTCTGATCTGATCTGATCTGATCTGCTTCCGCACTGCAAGCTGTTGTAATGAGAT 1003
DB 608 CCTCCGGAAGGAT 667
OY 1004 TCACTGTTGTAAGAGCTGATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
DB 668 TCGACTGTTGTAAGAGCTGATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
OY 1064 AGGAATACCGCCCAAGAGTTG 1088
DB 728 AGGCTCTCTGATCACTGATGATG 752

RESULT 13
A23646 1473 bp mRNA linear PAT 23-FEB-1995
LOCUS A23646 F. oxysporum endoglucanase gene.
DEFINITION A23646
ACCESSION A23646
VERSION A23646.1 GI:832892
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum

REFERENCE
AUTHORS 1 (bases 1 to 1473)
TITLE Conventis, A.C., Busch, A. and Baek, A.C.
JOURNAL Deletent compositions with high activity cellulase and quaternary ammonium compounds
Patent: EP 0495554-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY
FEATURES
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BASE COUNT 343 a 453 c 337 g 340 t

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
Best Local Similarity 59.5%; Pred. No. 8.3e-41;
Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

OY 464 GTGGTGCCTCTGTTAAGCGGTGCACTACTGTTATTGGGATTGCTTAAGGCTCTGTTA 523
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DB 203 CTGGAGCGGAAGGCTGCTGCAACGCCCTGCTTAACCTTGATGAAGAACCAACC 262
OY 584 CTGCGCTTAAGTACAGCAATGTCCAAAGTGTGTAACGCTGTAACAGTTACATGTGTA 643
DB 263 CCATTTCCACACCAATGTCTGTAACGCTGTAAGGCTGTAAGGCTGTAAGGCTGTA 322
OY 644 ACGAACACAGCTTGGGCTGTAACGATTAATCTTGGCTTATGCTGCTGCTGCA 703
DB 323 CCAACTACTCTCTGCGGCTGTAACGATTAATCTTGGCTTATGCTGCTGCTGCA 382
OY 704 TCAAGTGTGTTGTAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 763
DB 383 TCTCCGGTGTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 442
OY 764 CTTCTGTTGTTGTAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 823
DB 443 GCCCGTCAAGGCGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 501
OY 824 CCTCTACTGTTGCTCACTTGAATGCAATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 883
DB 502 -----GACAAACACTTCTGATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 553
OY 884 GTTCTCAAGCAATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 943
DB 554 GCTGCACTCTGAGTTGG-----CAAGGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 607
OY 944 CTTCTGATCTGATCTGATCTGATCTGCTTCCGCACTGCAAGCTGTTGTAATGAGAT 1003
DB 608 CCTCCGGAAGGAT 667
OY 1004 TCACTGTTGTAAGAGCTGATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
DB 668 TCGACTGTTGTAAGAGCTGATTAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 727

QY 1064 AGGAATCAACGCCAAGACAGTTG 1088
 DB 728 AGGCTCTCCTCGACATCAAGTGATG 752

RESULT 14
 A23955 / 1473 bp DNA linear PAT 01-MAR-1995
 LOCUS Endoglucanase gene.
 DEFINITION A23955
 ACCESSION A23955.1 GI:832896
 VERSION
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 Baech, A.C., Busch, A. and Ceulemans, R.A.A.
 Compact detergent compositions with high activity cellulase
 Patent: EP 0495257-A 3 22-JUL-1992;
 THE PROCTER & GAMBLE COMPANY
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BASE COUNT 343 a 453 c 337 g 340 t

ORIGIN

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
 Best Local Similarity 59.5%; Pred. No. 8.3e-41;
 Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

QY 464 GTGTGCTCTGTGTAAAGCGTGTCACTGCTTAATGGGATTGCTGAAGCCCTCTGTA 523
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QY 524 GGTGGCCGGTAAGCCCAATGTCACTTCTCTGTCAGTCTGTAAACGTTGTAACAGATGTGTCA 583
 DB 203 GTTGAAGCGGAAAGCGTGTCAACGCCCTGCTTAATGTGATAGAACACAACC 262

QY 584 CTGCCCTTAGTACAGCAATGTCCAAAGTGTGTAAAGCGTGTAAAGCGTGTAAAGTGTGA 643
 DB 263 CCAATTCCAACAACAATGTCTGTCAACGGTGTGAAGGTTGTCTGTATGTCTGTGA 322

QY 644 AGCAACAACAGCGTGGCGTGTAAAGCATATCTTGCTATGGTTCTGCTGTGCTGCA 703
 DB 323 CCAACTACTCTCTCTGGCGTGTCAACGATGAGCTTGGCTTCCCTGTCAACAGA 382

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QY 824 CTTCTACTGTGTGTCACTTGTGCAATGTCCGCGTGTGTGTGTGTGTGTGTGTGTGTGT 883
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QY 884 GTGTCTCAACGAATGGGGTGTCTCCCAATGACGTTGGGCTGTGAATACGTTGATTT 943
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QY 944 CTTTGTGATCTGACTGCTCTAGTCTTCTCCGACCTCAAGCGTGTGTGAATGAGAT 1003
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QY 1004 TCAACTGTTTCAAGAACGCTGATTAACCCAGCATGACTTACAGGAATTAACCTGTGCCA 1063
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QY 1064 AGGAATCAACGCCAAGACAGTTG 1088
 DB 728 AGGCTCTCCTCGACATCAAGTGATG 752

RESULT 15
 A23955 / 1473 bp DNA linear PAT 01-MAR-1995
 LOCUS Endoglucanase gene.
 DEFINITION A23955
 ACCESSION A23955.1 GI:832900
 VERSION
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 McCortqudale, F. and Busch, A.
 Dye transfer inhibiting compositions
 Patent: EP 0540784-A 3 12-MAY-1993;
 THE PROCTER & GAMBLE COMPANY
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BASE COUNT 343 a 453 c 337 g 340 t

ORIGIN

Query Match 17.6%; Score 194.2; DB 6; Length 1473;
 Best Local Similarity 59.5%; Pred. No. 8.3e-41;
 Matches 372; Conservative 0; Mismatches 238; Indels 15; Gaps 2;

QY 464 GTGTGCTCTGTGTAAAGCGTGTCACTGCTTAATGGGATTGCTGAAGCCCTCTGTA 523
 DB 143 GTGTGCTCTGTGTAAAGCGTGTCACTGCTTAATGGGATTGCTGAAGCCCTCTGCT 202

QY 524 GGTGGCCGGTAAGCCCAATGTCACTTCTCTGTCAGTCTGTAAACGTTGTAACAGATGTGTCA 583
 DB 203 GTTGAAGCGGAAAGCGTGTCAACGCCCTGCTTAATGTGATAGAACACAACC 262

QY 584 CTGCCCTTAGTACAGCAATGTCCAAAGTGTGTAAAGCGTGTAAAGCGTGTAAAGTGTGA 643
 DB 263 CCAATTCCAACAACAATGTCTGTCAACGGTGTGAAGGTTGTCTGTATGTCTGTGA 322

QY 644 AGCAACAACAGCGTGGCGTGTAAAGCATATCTTGCTATGGTTCTGCTGTGCTGCA 703
 DB 323 CCAACTACTCTCTCTGGCGTGTCAACGATGAGCTTGGCTTCCCTGTCAACAGA 382

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OY 704 TCAATGAGTGTGTAATCTGCTGAGTCTGTTCTGTTGAACTTACTTCACTTCTA 763
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OY 764 CTTCTGTGCTGTGTAAGATGTGTTATCAAGTCACTACACTGTGTGTGATCTGACT 823
Db 443 GCCCGGTCAAGGGCAGAGATGATCGTCCAGTCCACCAACACTGAGGTGATCTCGGC- 501
OY 824 CTTCTACTGTGCTCACTTGTACTTGTCAAAATGCCGGTGTGTGTGTGTGTATTTCAATG 883
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Db 554 GCTGCACCTCTGAGTTGG-----CAAGCTCTGGGGGTGCCAGTACGGGGTATCT 607
OY 944 CTTCTGATCTGACTGCTTGTCTTCTTCTTCCGCACTTCAAGCTGTGTGTGTGTGTGTGT 1003
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OY 1004 TCAACTGTGTCAAGAGCTGATATACCCAGCATGACTTACAGAGAGTTACTGTCCA 1063
Db 668 TCGACTGTGTGAGAGCGCCGACACCTGACTTCACTTGAAGAGGTTCAGTCCCCA 727
OY 1064 AGAAATCACCAGCCAGACAGTTG-1088
Db 728 AGGCTTCTTGTGACATCAGTGGATG 752
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